

Fig.1.

0411-wr MYSLVFVILMCIPIF-----SFOITVYDDK[SVC]-DS DNKEYHGI EVYVE A 42
 ckbp-lister --MKQYIVLACMLAAAMPASLQSSSSSSCTEE ENKH HGI DVYIIKV 48

 0411-wr TLOE--PLRQTTCESKIHKYGA-----VESEDDSTSVEDVDPTTYS 63
 ckbp-lister T K Q D O T P T N D K I C O S V T E I T E S E S D P D P E V E S E D D S T S V E D V D P P T T Y S 98

 0411-wr V S N G G L N I S V D L N C F L N F H T V G V Y T N R D T V Y A K F A S L O P W T T E P I N S M T 113
 ckbp-lister I I G G G L R M N F G F T K C - P O I K S I S E S A D G N T V N A R L S S V S P G G K O S P A I T 147

 0411-wr H D D L V K L T E C I V D I Y L K C E V D K T K D F M K T I N G N R L K P R D F K T V P P S N V G S 183
 ckbp-lister R E E A L A M I K O C E V S I D I R C S E E K D S D I K I H P V L G S N I S H K K V S Y E D I I G 197

 0411-wr M I E L O S O Y C V N D V T Y Y K I Y D E C G N I K O H S I P T L R D Y F T T K N G - - - - - 206
 ckbp-lister S T I V D T K - C V K N L E F S V R I G D M C - - - K E S S E L E V K D G F K Y Y V D G S A S E G A T 243

 0411-wr - O P R K I L K K F D N C -
 ckbp-lister D O T S L I D S T K L K A C V 219
 258

Fig.2.

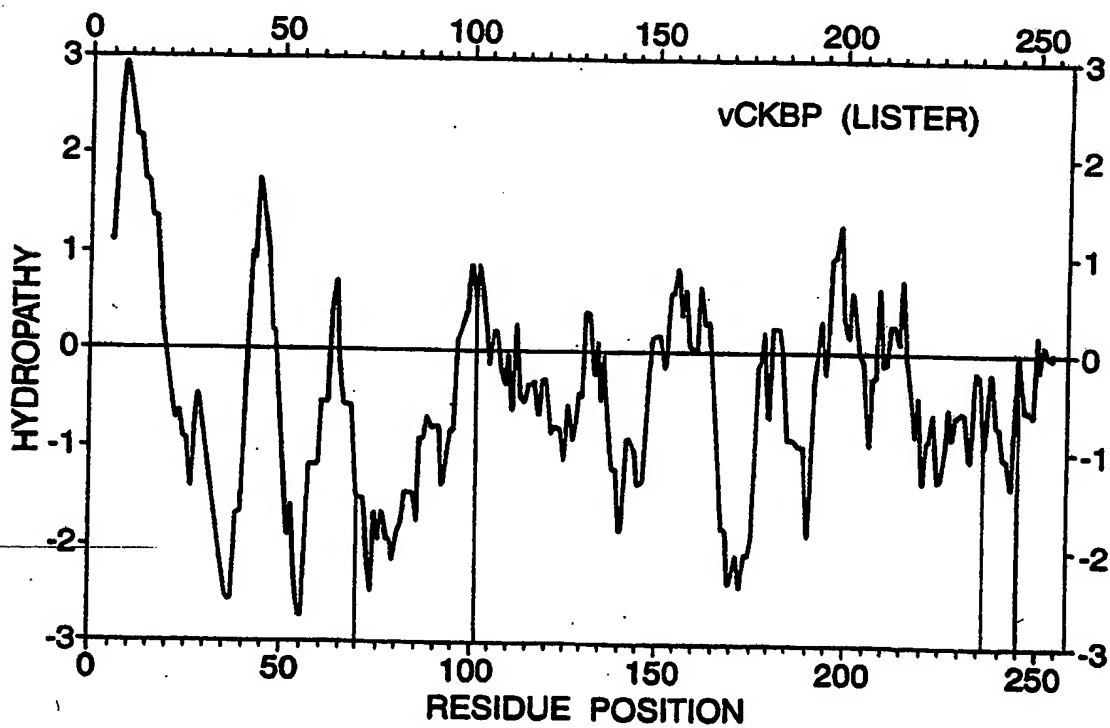
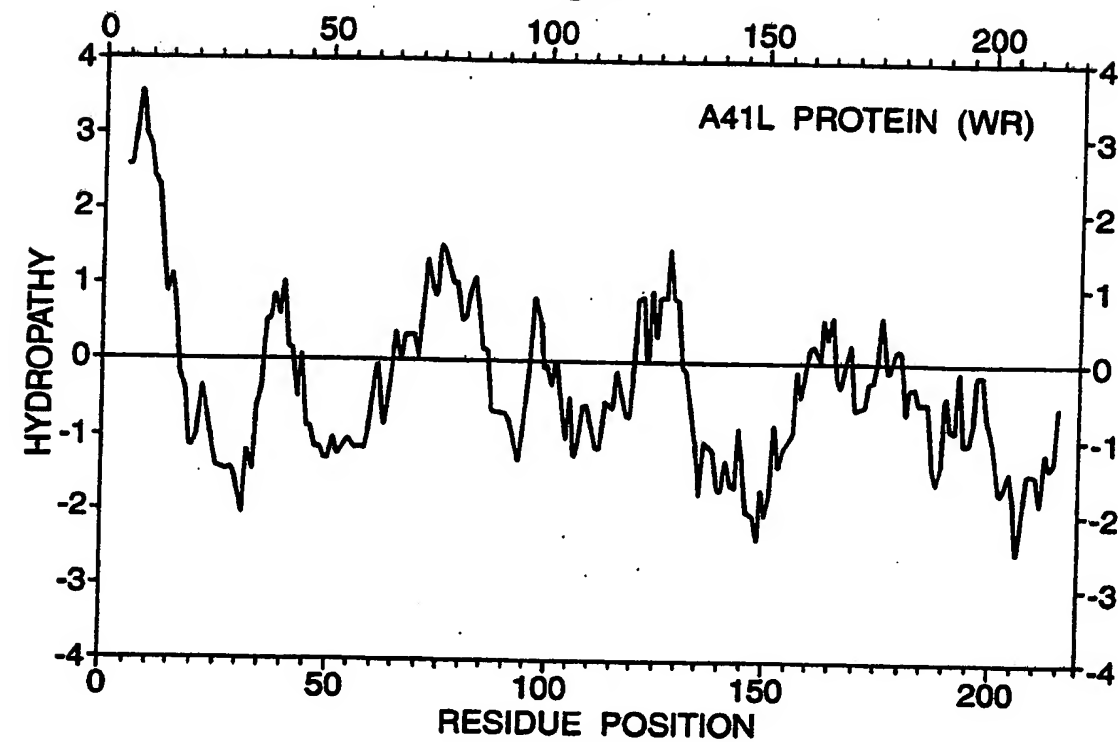


Fig.3.

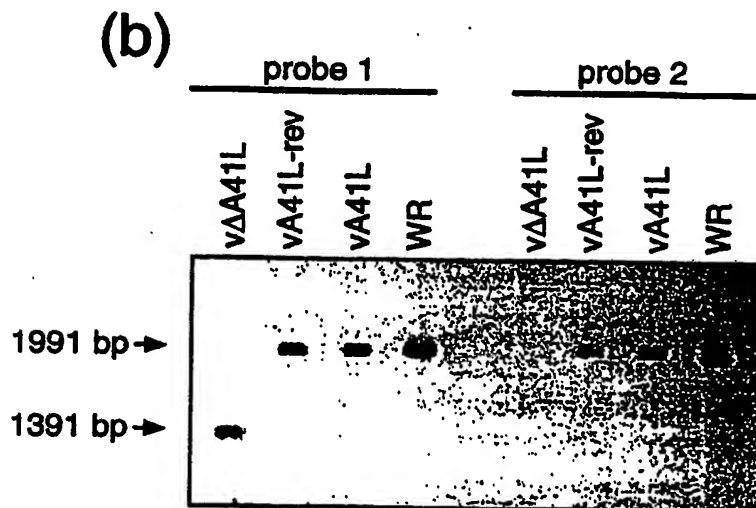
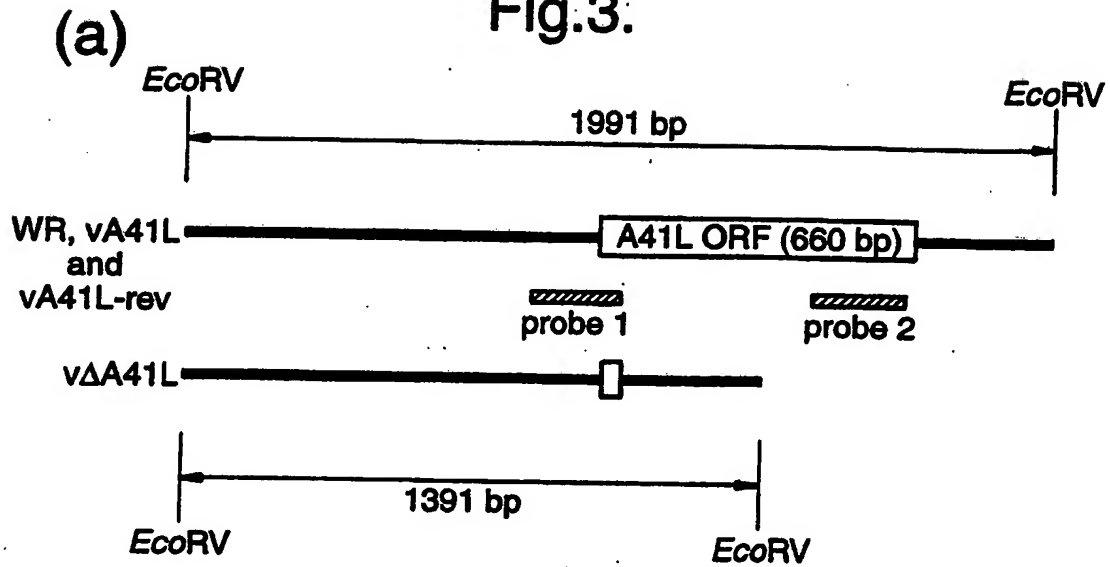
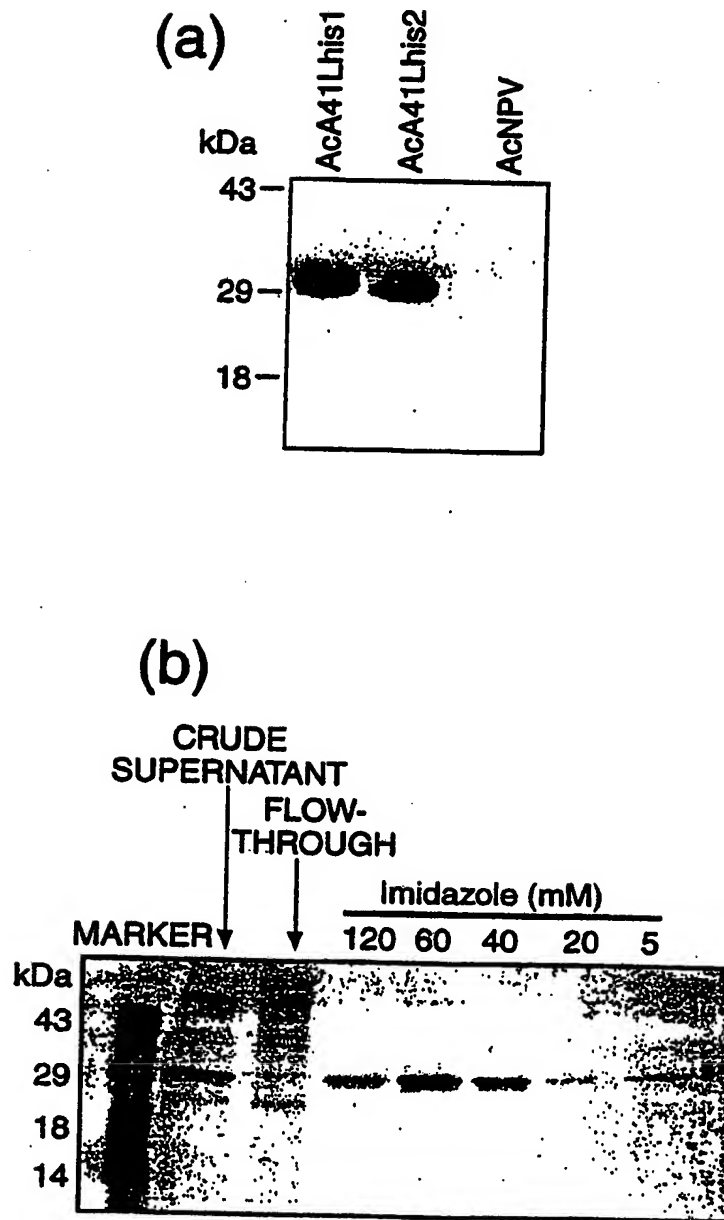


Fig.4.



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Fig.5.

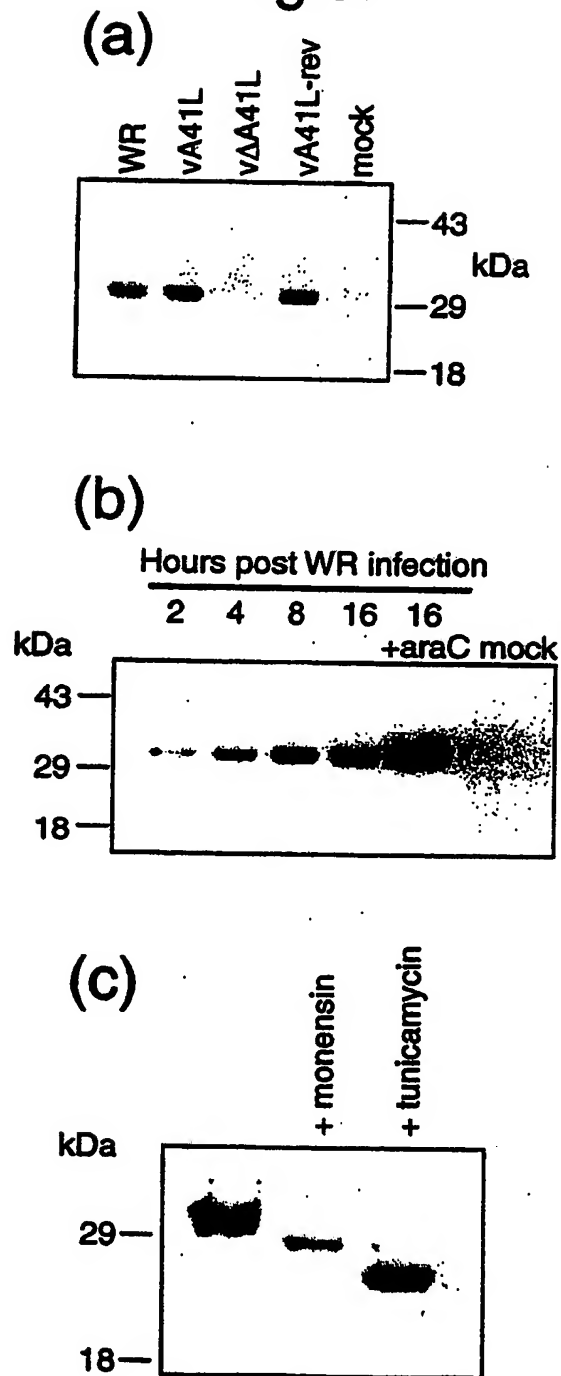


Fig.6.

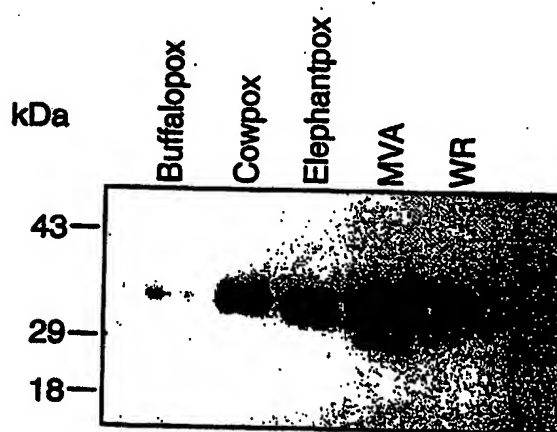
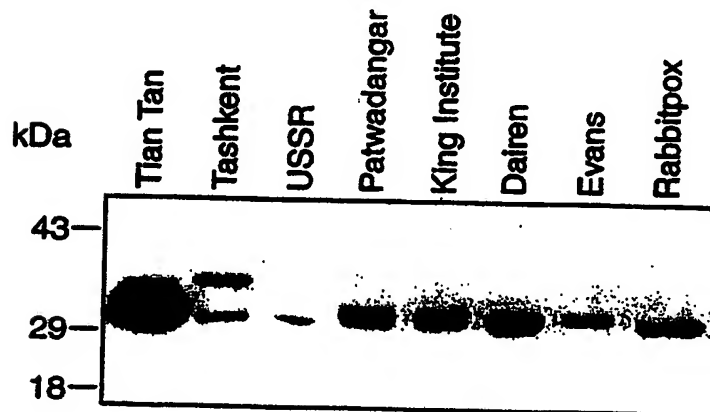
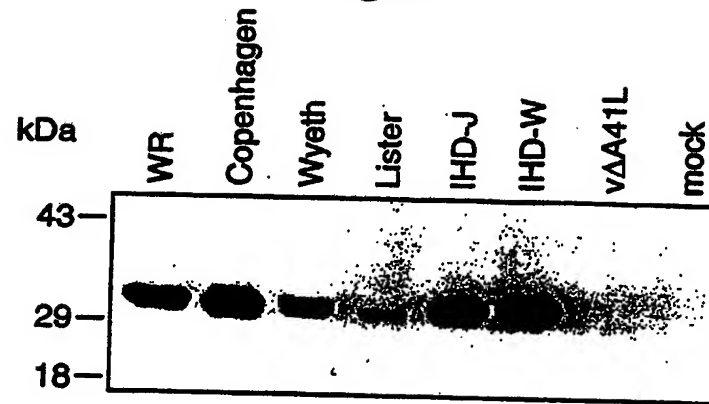


Fig.7(a).

CXC CHEMOKINES

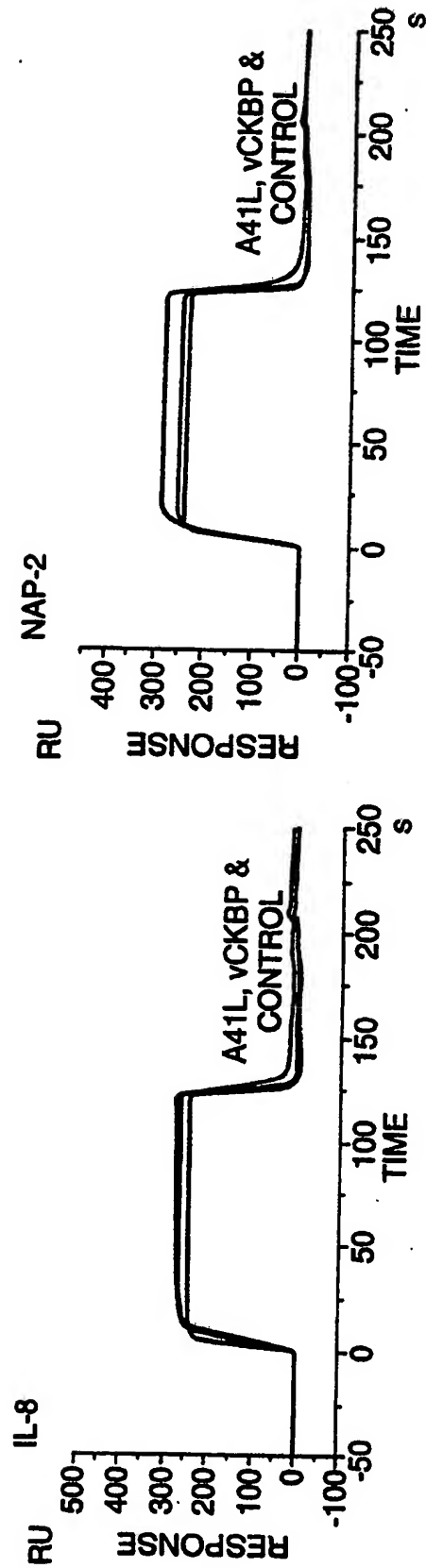
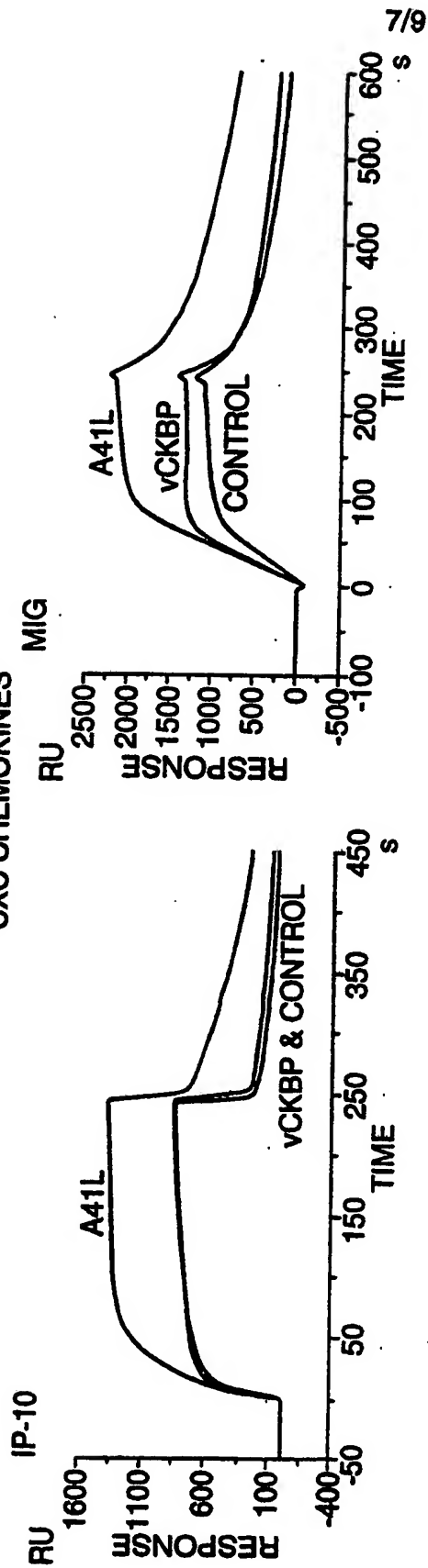


Fig.7(b).

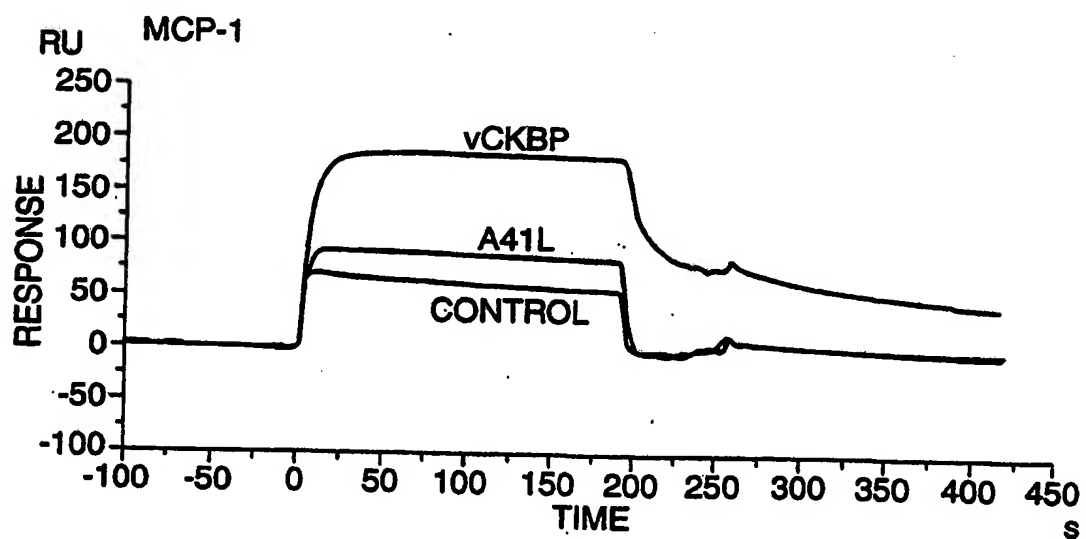
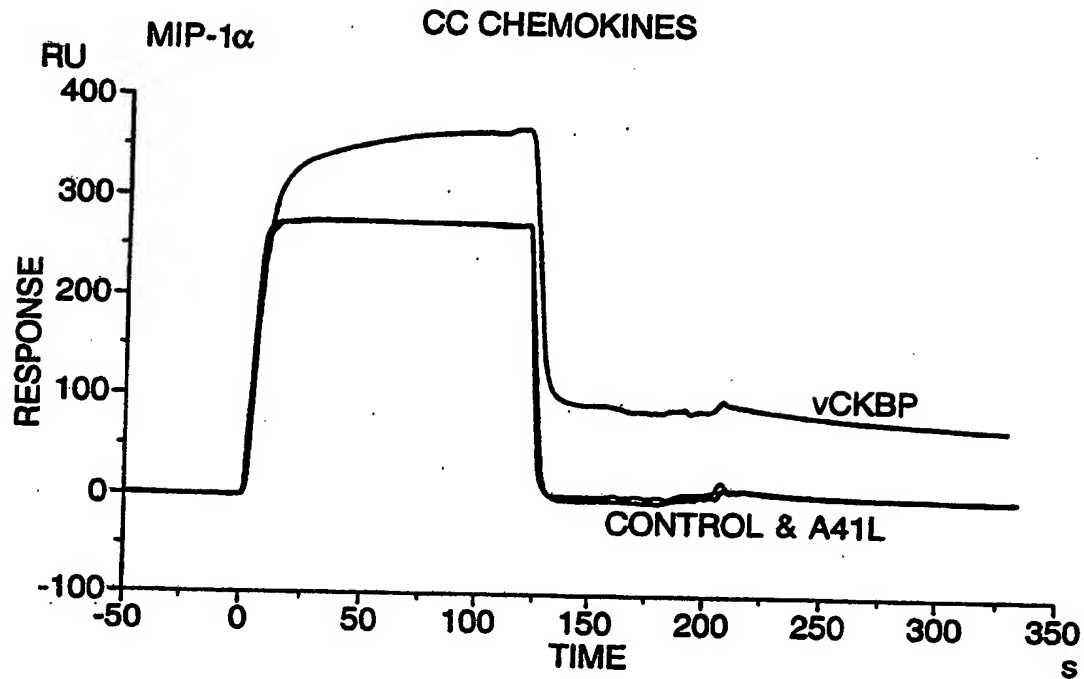


Fig.8.

1 AAACTTGACA TTAGCATTTT ATTCTTATTA CAAAATATAA AATAAAATAT
51 ACAATCCAAT ACTCACATAA TCCAAC TCAC TCGAACACTA TTTTTCCAAT
101 TACGATAACA ATATTGCAGA ATGTACTCGT TAGTATTTGT TATTTTGATG
151 TGTATACCAT TTAGTTTICA AACAGTGTAT GATGATAAAT CGGTATGCGA
201 TTCTGACAAT AAAGAATATA TGGGAATAGA AGTTTATGTA GAAGCAACGC
251 TAGACGAACC CCTCAGACAA ACAACGTGTG AATCCAAAAT CCATAAATAT
301 GGTGCATCTG TATCAAACGG AGGATTAAAT ATTTCTGTTG ATCTATTAAA
351 CTGTTTTCTT AATTTTCATA CAGTTGGTGT ATACACTAAT CGCGATACCG
401 TATACGCGAA GTTTGCTAGT TTGGATCCAT GGACTACGGA ACCTATAAAT
451 TCTATGACCC ATGACGATCT AGTAAAATTA ACAGAAGAAT GTATAGTGGA
501 CATTTATTTA AAATGTGAAG TGGATAAAAC AAAGGATTTC ATGAAAAC TA
551 ACGGTAATAG ATTAAAACCA AGAGACTTTA AAACTGTTCC TCCTTCTAAT
601 GTAGGAAGCA TGATAGAACT ACAGTCTGAC TATTGCGTAA ACGATGTGAC
651 TACATACGTC AAAATATACG ATGAGTGTGG AAACATTAAA CAGCATTCCA
701 TTCCAACACT AAGAGATTAT TTACCACCA AGAATGGTCA ACCACGTAAA
751 ATATTAAAGA AAAAATTGA TAATTGTTAA TTGTTATTTT TATAAAAACA
801 AGAACGGTAC GGCGATATTT ATTTTTTCT AAAACATCTA ACCGAAGTAG
851 TGGTATGATA AAAATGTAGT GTAATTGTTA TATAGTGTA CACGAAT